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Lys	Glu	Leu	Ile	Asp	Thr	Leu	Asp	Ala	G1u	Thr	Thr	Pro	Lys	Ile	Leu	
	200					205					210					
gtg	aat	aca	ttt	gat	gaa	tta	gag	cct	gag	gca	ctc	aat	gca	att	gaa	1030
Val	Asn	Thr	Phe	Asp	Glu	Leu	G1u	Pro	G1u	Ala	Leu	Asn	Ala	Ile	G1u	
215					220					225					230	
ggt	tat	aag	ttt	tat	gga	att	gga	ccg	ttg	att	cct	tct	gct	ttc	ttg	1078
					G1y											
-	-	-		235	_				240					245		

ggt	gga	aat	gac	cct	tta	gat	gct	tca	ttt	ggt	ggt	gat	ctt	ttt	caa	1126
G1y	Gly	Asn	Asp	Pro	Leu	Asp	Ala	Ser	Phe	Gly	Gly	Asp	Leu	Phe	Gln	
			250					255					260			
aat	tca	aat	gac	tat	atg	gaa	tgg	tta	aac	tca	aag	cca	aat	tca	tca	1174
Asn	Ser	Asn	Asp	Tyr	Met	G1u	Trp	Leu	Asn	Ser	Lys	Pro	Asn	Ser	Ser	
		265					270					275				
gtt	gtt	tat	ata	tct	ttt	ggg	agt	cta	atg	aat	cca	tct	att	agc	caa	1222
Val	Va1	Tyr	11e	Ser	Phe	Gly	Ser	Leu	Met	Asn	Pro	Ser	I1e	Ser	Gln	
	280					285					290					
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Met	Glu	G1u	Ile	Ser	Lys	Gly	Leu	Ile	Asp	Ile	Gly	Arg	Pro	Phe	Leu	
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Trp	Val	Ile	Lys	Glu	Asn	G1u	Lys	Gly	Lys	Glu	Glu	Glu	Asn	Lys	Lys	
				315					320					325		
ctt	ggt	tgt	at.t	gaa	gaa	ttg	gaa	aaa	ata	gga	aaa	ata	gtt	cca	tgg	1366
Leu	Gly	Cys	Ile	Glu	Glu	Leu	G1u	Lys	Ile	G1y	Lys	Ile	Va1	Pro	Trp	
			330					335					340			
tgt	tca	caa	ctt	gaa	gtt	cta	aaa	cat	cca	tct	tta	gga	tgt	ttt	gtt	1414
Cys	Ser	Gln	Leu	Glu	Va1	Leu	Lys	His	Pro	Ser	Leu	G1y	Cys	Phe	Val	
		345					350					355				
tct	cat	tgt	gga	tgg	aat	tca	gcc	tta	gag	agt	tta	gct	tgt	gga	gtg	1462
Ser	His	Cys	Gly	Trp	Asn	Ser	Ala	Leu	G1u	Ser	Leu	Ala	Cys	Gly	Val	
	360					365					370					
cca	gtt	gtg	gca	ttt	cct	caa	tgg	aca	gat	caa	atg	aca	aat	gcc	aaa	1510
Pro	Va1	Va1	Ala	Phe	Pro	G1n	Trp	Thr	Asp	Gln	Met	Thr	Asn	Ala	Lys	
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caa	gtt	gaa	gat	gtg	tgg	aaa	agt	gga	gta	aga	gtg	aga	ata	aat	gaa	1558
G1n	Va1	Glu	Asp	Val	Trp	Lys	Ser	Gly	Val	Arg	Val	Arg	Ile	Asn	G1u	
				395					400					405		
gat	ggt	gtt	gtt	gaa	agt	gag	gaa	atc	aaa	agg	tgt	att	gaa	ttg	gta	1606
Asp	G1y	Va1	Va1	Glu	Ser	Glu	Glu	Ile	Lys	Arg	Cys	Ile	Glu	Leu	Val	
			410					415					420			
atg	gat	gga	gga	gag	aaa	ggg	gaa	gaa	ttg	aga	aag	aat	gct	aag	aaa	1654
Met	Asp	Gly	G1y	Glu	Lys	Gly	G1u	Glu	Leu	Arg	Lys	Asn	Ala	Lys	Lys	
		425					430					435				

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Trp Lys Glu Leu Ala Arg Glu Ala Val Lys Glu Gly Gly Ser Ser His
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aag aat tta aag gct ttt att gat gat gtt gcc aaa ggg ttt taatatttac 1754
Lys Asn Leu Lys Ala Phe Ile Asp Asp Val Ala Lys Gly Phe
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                    460
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Asp Val Thr Phe Phe Thr Ser Val Tyr Ala Trp Arg Arg Met Ala Asn
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Thr Ala Ser Ala Ala Ala Gly Asn Pro Pro Gly Leu Asp Phe Val Ala
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Phe Ser Asp Gly Tyr Asp Asp Gly Leu Lys Pro Cys Gly Asp Gly Lys
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Arg Tyr Met Ser Glu Met Lys Ala Arg Gly Ser Glu Ala Leu Arg Asn
Leu Leu Leu Asn Asn His Asp Val Thr Phe Val Val Tyr Ser His Leu
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Phe Ala Trp Ala Ala Glu Val Ala Arg Glu Ser Gln Val Pro Ser Ala
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                            120
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Leu Leu Trp Val Glu Pro Ala Thr Val Leu Cys Ile Tyr Tyr Phe Tyr
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                        135
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145					150					155					160
Leu	Pro	Arg	Leu	Pro	Pro	Leu	G1u	Gln	Arg	Ser	Leu	Pro	Thr	Phe	Leu
				165					170					175	
Leu	Pro	G1u	Thr	Pro	G1u	Arg	Phe	Arg	Leu	Met	Met	Lys	G1u	Lys	Leu
			180					185					190		
Glu	Thr	Leu	Asp	Gly	G1u	G1u	Lys	Ala	Lys	Val	Leu	Val	Asn	Thr	Phe
		195					200					205			
Asp	Ala	Leu	Glu	Pro	Asp	Ala	Leu	Thr	Ala	Ile	Asp	Arg	Tyr	G1u	Leu
	210					215					220				
Ile	G1y	Ile	G1y	Pro	Leu	Ile	Pro	Ser	Ala	Phe	Leu	Asp	Gly	G1y	Asp
225					230					235					240
Pro	Ser	Glu	Thr	Ser	Tyr	G1y	G1y	Asp	Leu	Phe	G1u	Lys	Ser	Glu	Glu
				245					250					255	
Asn	Asn	Cys	Va1	Glu	Trp	Leu	Asp	Thr	Lys	Pro	Lys	Ser	Ser	Va1	Va1
			260					265					270		
Tyr	Val	Ser	Phe	Gly	Ser	Val	Leu	Arg	Phe	Pro	Lys	Ala	G1n	Met	G1u
		275					280					285			
G1u	Ile	Gly	Lys	G1y	Leu	Leu	Ala	Cys	Gly	Arg	Pro	Phe	Leu	Trp	Met
	290					295					300				
lle	Arg	G1u	G1n	Lys	Asn	Asp	Asp	Gly	Glu	Glu	Glu	Glu	G1u	Glu	Leu
305					310					315					320
Ser	Cys	Ile	Gly	Glu	Leu	Lys	Lys	Met	Gly	Lys	Ile	Va1	Ser	Trp	Cys
				325					330					335	
Ser	G1n	Leu	Glu	Va1	Leu	Ala	His	Pro	Ala	Leu	Gly	Cys	Phe	Val	Thr
			340					345					350		
His	Cys	Gly	Trp	Asn	Ser	A1a	Val	G1u	Ser	Leu	Ser	Cys	Gly	Val	Pro
		355					360					365			
Va1	Val	Ala	Va1	Pro	Gln	Trp	Phe	Asp	Gln	Thr	Thr	Asn	Ala	Lys	Leu
	370			•		375					380				
Ile	G1u	Asp	Ala	Trp	G1y	Thr	Gly	Val	Arg	Val	Arg	Met	Asn	Glu	Gly
385					390					395					400
G1y	G1y	Va1	Asp	Gly	Ser	Glu	Ile	G1u	Arg	Cys	Val	G1u	Met	Val	Met
				405					410					415	

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Asp Gly Gly Glu Lys Ser Lys Leu Val Arg Glu Asn Ala Ile Lys Trp
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Lys Thr Leu Ala Arg Glu Ala Met Gly Glu Asp Gly Ser Ser Leu Lys
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Asp Val Thr Phe Phe Thr Ser Val Tyr Ala Trp Arg Arg Met Ala Asn
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Thr Ala Ser Ala Ala Ala Gly Asn Pro Pro Gly Leu Asp Phe Val Ala
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Phe Ser Asp Gly Tyr Asp Asp Gly Leu Lys Pro Gly Gly Asp Gly Lys
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Arg Tyr Met Ser Glu Met Lys Ala Arg Gly Ser Glu Ala Leu Arg Asn
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Leu Leu Leu Asn Asn Asp Asp Val Thr Phe Val Val Tyr Ser His Leu
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Phe Ala Trp Ala Ala Glu Val Ala Arg Leu Ser His Val Pro Thr Ala
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Leu Leu Trp Val Glu Pro Ala Thr Val Leu Cys Ile Tyr His Phe Tyr
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Phe Asn Gly Tyr Ala Asp Glu Ile Asp Ala Gly Ser Asn Glu Ile Gln
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Leu Pro Arg Leu Pro Ser Leu Glu Gln Arg Ser Leu Pro Thr Phe Leu
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Leu Pro Ala Thr Pro Glu Arg Phe Arg Leu Met Met Lys Glu Lys Leu
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                                 185
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Glu Thr Leu Asp Gly Glu Glu Lys Ala Lys Val Leu Val Asn Thr Phe
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                            200
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Asp Ala Leu Glu Pro Asp Ala Leu Thr Ala Ile Asp Arg Tyr Glu Leu
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Ile Gly Ile Gly Pro Leu Ile Pro Ser Ala Phe Leu Asp Gly Glu Asp
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                                        235
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Pro Ser Glu Thr Ser Tyr Gly Gly Asp Leu Phe Glu Lys Ser Glu Glu
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Asn Asn Cys Val Glu Trp Leu Asn Ser Lys Pro Lys Ser Ser Val Val
                                265
Tyr Val Ser Phe Gly Ser Val Leu Arg Phe Pro Lys Ala Gln Met Glu
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                            280
                                                285
Glu Ile Gly Lys Gly Leu Leu Ala Cys Gly Arg Pro Phe Leu Trp Met
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Ile Arg Glu Gln Lys Asn Asp Asp Gly Glu Glu Glu Glu Glu Glu
                                                            320
                    310
                                        315
Glu Leu Ser Cys Ile Gly Glu Leu Lys Lys Met Gly Lys Ile Val Ser
                                    330
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Trp Cys Ser Gln Leu Glu Val Leu Ala His Pro Ala Leu Gly Cys Phe
                                345
Val Thr His Cys Gly Trp Asn Ser Ala Val Glu Ser Leu Ser Cys Gly
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Ile Pro Val Val Ala Val Pro Gln Trp Phe Asp Gln Thr Thr Asn Ala
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Lys Leu Ile Glu Asp Ala Trp Gly Thr Gly Val Arg Val Arg Met Asn
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Glu Gly Gly Val Asp Gly Cys Glu Ile Glu Arg Cys Val Glu Met
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Val Met Asp Gly Gly Asp Lys Thr Lys Leu Val Arg Glu Asn Ala Ile
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Ile	Asn	Pro	Ala	Leu	G1n	Phe	Ala	Lys	Arg	Leu	Ala	Asn	Ala	Asp	Ile
		-	20					25					30		
Gln	Va1	Thr	Phe	Phe	Thr	Ser	Val	Tyr	Ala	Trp	Arg	Arg	Met	Ser	Arg
		35					40					45			
Thr	Ala	Ala	G1y	Ser	Asn	G1y	Leu	Ile	Asn	Phe	Val	Ser	Phe	Ser	Asp
	50					55					60				
Gly	Tyr	Asp	Asp	G1y	Leu	Gln	Pro	Gly	Asp	Asp	Gly	Lys	Asn	Tyr	Met
65					70					75					80
Ser	Glu	Met	Lys	Ser	Arg	G1y	Ile	Lys	Ala	Leu	Ser	Asp	Thr	Leu	Ala
				85					90					95	
Ala	Asn	Asn	Va1	Asp	G1n	Lys	Ser	Ser	Lys	Ile	Thr	Phe	Val	Va1	Tyr
			100					105					110		
Ser	His	Leu	Phe	Ala	Trp	Ala	Ala	Lys	Val	Ala	Arg	Glu	Phe	His	Leu
		115					120					125			
Arg	Ser	Ala	Leu	Leu	Trp	Ile	Glu	Pro	Ala	Thr	Val	Leu	Asp	Ile	Phe
	130					135					140				
Tyr	Phe	Tyr	Phe	Asn	Gly	Tyr	Ser	Asp	Glu	Ile	Asp	Ala	Gly	Ser	Asp
145					150					155					160
Ala	Ile	His	Leu	Pro	G1y	Gly	Leu	Pro	Val	Leu	Ala	G1n	Arg	Asp	Leu
				165					170					175	
Pro	Ser	Phe	Leu	Leu	Pro	Ser	Thr	His	Glu	Arg	Phe	Arg	Ser	Leu	Met
			180					185					190		
Lys	G1u	Lys	Leu	Glu	Thr	Leu	Glu	Gly	Glu	Glu	Lys	Pro	Lys	Val	Leu
		195					200					205			
Va1	Asn	Ser	Phe	Asp	Ala	Leu	G1u	Pro	Asp	Ala	Leu	Lys	A1a	Ile	Asp
	210					215					220				
Lys	Tyr	Glu	Met	Ile	Ala	Ile	Gly	Pro	Leu	Ile	Pro	Ser	Ala	Phe	Leu
225					230					235					240
Asp	Gly	Lys	Asp	Pro	Ser	Asp	Arg	Ser	Phe	Gly	G1y	Asp	Leu	Phe	Glu
				245					250					255	
Lys	G1y	Ser	Asn	Asp	Asp	Asp	Cys	Leu	Glu	Trp	Leu	Ser	Thr	Asn	Pro
			260					265					270		

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Arg Ser Ser Val Val Tyr Val Ser Phe Gly Ser Phe Val Asn Thr Thr
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                            280
Lys Ser Gln Met Glu Glu Ile Ala Arg Gly Leu Leu Asp Cys Gly Arg
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                                            300
Pro Phe Leu Trp Val Val Arg Val Asn Glu Gly Glu Glu Val Leu Ile
                                        315
305
                    310
Ser Cys Met Glu Glu Leu Lys Arg Val Gly Lys Ile Val Ser Trp Cys
                                    330
                325
Ser Gln Leu Glu Val Leu Thr His Pro Ser Leu Gly Cys Phe Val Thr
                                345
His Cys Gly Trp Asn Ser Thr Leu Glu Ser Ile Ser Phe Gly Val Pro
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                            360
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Met Val Ala Phe Pro Gln Trp Phe Asp Gln Gly Thr Asn Ala Lys Leu
                        375
Met Glu Asp Val Trp Arg Thr Gly Val Arg Val Arg Ala Asn Glu Glu
                                        395
                                                            400
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Gly Ser Val Val Asp Gly Asp Glu Ile Arg Arg Cys Ile Glu Glu Val
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                                    410
Met Asp Gly Glu Lys Ser Arg Lys Leu Arg Glu Ser Ala Gly Lys
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Trp Lys Asp Leu Ala Arg Lys Ala Met Glu Glu Asp Gly Ser Ser Val
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Tyr	Val	Asp	Gln	Val	Thr	Phe	Phe	Thr	Ser	Va1	Tyr	Ala	Leu	Arg	Arg
		35					40					45			
Met	Arg	Phe	Glu	Thr	Asp	Pro	Ser	Ser	Arg	Ile	Asp	Phe	Val	Ala	Xaa
	50					55					60				
Xaa	Asp	Ser	Tyr	Asp	Asp	Gly	Leu	Lys	Lys	Gly	Asp	Asp	Gly	Lys	Asn
65					70					75					80
Tyr	Met	Ser	G1u	Met	Arg	Lys	Arg	G1y	Thr	Lys	Ala	Leu	Lys	Asp	Thr
				85					90					95	
Leu	Ile	Lys	Leu	Asn	Asp	Ala	Ala	Met	Gly	Ser	Glu	Cys	Tyr	Asn	Arg
			100					105					110		
Val	Ser	Phe	Val	Va1	Tyr	Ser	His	Leu	Phe	Ser	Trp	Ala	Ala	Glu	Val
		115					120					125			
Ala	Arg	G1u	Val	Asp	Va1	Pro	Ser	Ala	Leu	Leu	Trp	Ile	G1u	Pro	Ala
	130					135					140				
Thr	Val	Phe	Asp	Val	Tyr	Tyr	Phe	Tyr	Phe	Asn	Gly	Tyr	Ala	Asp	Asp
145					150					155					160
I1e	Asp	Ala	Gly	Ser	Asp	Gln	Ile	G1n	Leu	Pro	Asn	Leu	Pro	Gln	Leu
				165					170					175	
Ser	Lys	Gln	Asp	Leu	Pro	Ser	Phe	Leu	Leu	Pro	Ser	Ser	Pro	Ala	Arg
			180					185					190		
Phe	Arg	Thr	Leu	Met	Lys	G1u	Lys	Phe	Asp	Thr	Leu	Asp	Lys	G1u	Pro
		195					200					205			
Lys	Ala	Lys	Va1	Leu	Ile	Asn	Thr	Phe	Asp	Ala	Leu	G1u	Thr	G1u	Gln
	210					215					220				
Leu	Lys	Ala	Ile	Asp	Arg	Tyr	G1u	Leu	Ile	Ser	Ile	G1y	Pro	Leu	Ile
225					230					235					240
Pro	Ser	Ser	Ile	Phe	Ser	Asp	G1y	Asn	Asp	Pro	Ser	Ser	Ser	Asn	Lys
				245					250					255	
Ser	Tyr	Gly	Gly	Asp	Leu	Phe	Arg	Lys	Ala	Asp	Glu	Thr	Tyr	Met	Asp
			260					265					270		
Trp	Leu	Asn	Ser	Lys	Pro	Glu	Ser	Ser	Val	Va1	Tyr	Val	Ser	Phe	Gly
		275					280					285			

Ser	Leu	Leu	Arg	Leu	Pro	Lys	Pro	G1n	Met	Glu	Glu	Ile	Ala	Ile	Gly
	290					295					300				
Leu	Ser	Asp	Thr	Lys	Ser	Pro	Va1	Leu	Trp	Val	Ile	Arg	Arg	Asn	Glu
305					310					315					320
G1u	G1y	Asp	Glu	G1n	G1u	G1n	A1a	G1u	Glu	Glu	Glu	Lys	Leu	Leu	Ser
				325					330					335	
Phe	Phe	Asp	Arg	His	G1y	Thr	Glu	Arg	Leu	G1y	Lys	Ile	Val	Thr	Trp
			340					345					350		
Cys	Ser	Gln	Leu	Asp	Va1	Leu	Thr	His	Lys	Ser	Val	Gly	Cys	Phe	Val
		355					360					365			
Thr	His	Cys	Gly	Trp	Asn	Ser	Ala	Ile	Glu	Ser	Leu	Ala	Cys	G1y	Va1
	370					375					380				
Pro	Va1	Va1	Cys	Phe	Pro	Gln	Trp	Phe	Asp	Gln	G1y	Thr	Asn	Ala d	Lys
385					390					395					400
Met	Ile	G1u	Asp	Val	Trp	Arg	Ser	G1y	Va1	Arg	Val	Arg	Va1	Asn	Glu
				405					410					415	
Glu	G1y	Gly	Val	Val	Asp	Arg	Arg	Glu	Ile	Lys	Arg	Cys	Val	Ser	Glu
			420					425					430		
Va1	11e	Lys	Ser	Arg	G1u	Leu	Arg	Glu	Ser	Ala	Met	Met	Trp	Lys	Gly
		435					440					445			
Leu	A1a	Lys	G1u	Ala	Met	Asp	G1u	G1u	Arg	G1y	Ser	Ser	Met	Asn	Asn
	450					455					460				
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			20					25					30		
Ala	Ile	Met	Thr	Phe	Ser	Ala	Ser	Leu	Va1	Ser	Thr	Thr	Va1	Asp	Ala
		35					40					45			

Pro	Leu	Thr	Met	Ser	Phe	Thr	Thr	Tyr	Thr	Va1	Val	Ala	Leu	Leu	Tyr
	50					55					60				
G1y	Thr	Ile	Leu	Leu	Tyr	Arg	Arg	His	Lys	Phe	Leu	Val	Pro	Trp	Tyr
65					70					75					80
Trp	Tyr	Ala	Leu	Leu	G1y	Phe	Val	Asp	Val	His	G1y	Asn	Tyr	Leu	Val
				85					90					95	
Asn	Lys	Ala	Phe	Glu	Leu	Thr	Ser	11e	Thr	Ser	Val	Ser	Ile	Leu	Asp
			100					105					110		
Cys	Trp	Thr	Ile	Va1	Trp	Ser	Ile	Ile	Phe	Thr	Trp	Met	Phe	Leu	G1y
		115					120					125			
Thr	Lys	Tyr	Ser	Val	Tyr	Gln	Phe	Val	Gly	Ala	Ala	Ile	Cys	Va1	Gly
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Gly	Leu	Leu	Leu	Va1	Leu	Leu	Ser	Asp	Ser	Gly	Val	Thr	Ala	Ala	G1y
145					150					155					160
Ser	Asn	Pro	Leu	Leu	Gly	Asp	Phe	Leu	Val	Ile	Thr	Gly	Ser	Ile	Leu
				165					170					175	
Phe	Thr	Leu	Ser	Thr	Val	G1y	Gln	G1u	Tyr	Cys	Val	Lys	Arg	Lys	Asp
			180					185					190		
Arg	Ile	Glu	Va1	Val	Ala	Met	Ile	Gly	Va1	Phe	Gly	Met	Leu	Ile	Ser
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Ala	Thr	Glu	Ile	Thr	Val	Leu	Glu	Arg	Asn	Ala	Leu	Ser	Ser	Met	Gln
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Trp	Ser	Thr	G1y	Leu	Leu	Ala	Ala	Tyr	Va1	Val	Tyr	Ala	Leu	Ser	Ser
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Phe	Leu	Phe	Cys	Thr	Leu	Thr	Pro	Phe	Leu	Leu	Lys	Met	Ser	Gly	Ala
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Ala	Phe	Phe	Asn	Leu	Ser	Met	Leu	Thr	Ser	Asp	Met	Trp	Ala	Val	Ala
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I1e	Arg	Thr	Phe	Ile	Tyr	Asn	G1n	G1u	Val	Asp	Trp	Leu	Tyr	Tyr	Leu
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Glu	Val	Thr	Phe	Ser	Thr	Ser	Ile	Tyr	Ala	G1n	Ser	Arg	Met	Asp	G1u
		35					40					45			
Lys	Ser	Ile	Leu	Asn	Ala	Pro	Lys	Gly	Leu	Asn	Phe	Ile	Pro	Phe	Ser
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Asp	G1y	Phe	Asp	Glu	Gly	Phe	Asp	His	Ser	Lys	Asp	Pro	Va1	Phe	Tyr
65					70					75					80
Met	Ser	G1n	Leu	Arg	Lys	Cys	Gly	Ser	Glu	Thr	Val	Lys	Lys	Ile	I1e
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Leu	Thr	Cys	Ser	Glu	Asn	G1y	G1n	Pro	Ile	Thr	Cys	Leu	Leu	Tyr	Ser
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Ile	Phe	Leu	Pro	Trp	Ala	Ala	Glu	Val	Ala	Arg	G1u	Va1	His	Ile	Pro
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	130					135					140				
Phe	Asn	Phe	His	Gly	Tyr	Glu	Lys	Ala	Met	Ala	Asn	Glu	Ser	Asn	Asp
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Pro	Asn	Trp	Ser	Ile	Gln	Leu	Pro	Gly	Leu	Pro	Leu	Leu	G1u	Thr	Arg
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Gly	Gly	Asp	Leu	Phe	Gln	Asn	Ser	Asn	Asp	Tyr	Met	G1u	Trp	Leu	Asn
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Gly	Lys	Ile	Val	Pro	Trp	Cys	Ser	Gln	Leu	G1u	Va1	Leu	Lys	His	Pro
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Ser	Leu	Gly	Cys	Phe	Val	Ser	His	Cys	G1y	Trp	Asn	Ser	Ala	Leu	Glu
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Ser	Leu	Ala	Cys	G1y	Val	Pro	Val	Va1	Ala	Phe	Pro	G1n	Trp	Thr	Asp
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G1n 385		Thr	Asn	Ala	Lys 390		Val	Glu	Asp	Val 395		Lys	Ser	G1y	Va1 400
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385	Met				390	Gln				395	Trp				400
385 Arg	Met Val	Arg	Ile	Asn 405	390 Glu	Gln	Gly	Val	Val 410	395 Glu	Trp	Glu	Glu	Ile 415	400 Lys
385 Arg	Met Val	Arg	Ile	Asn 405	390 Glu	Gln Asp	Gly	Val	Val 410	395 Glu	Trp	Glu	Glu	Ile 415	400 Lys
385 Arg Arg	Met Val Cys	Arg Ile	Ile Glu 420	Asn 405 Leu	390 Glu Val	Gln Asp	Gly Asp	Val Gly 425	Val 410 Gly	395 Glu Glu	Trp Ser Lys	Glu Gly	Glu Glu 430	Ile 415 Glu	400 Lys Leu
385 Arg Arg	Met Val Cys	Arg Ile	Ile Glu 420	Asn 405 Leu	390 Glu Val	Gln Asp Met	Gly Asp	Val Gly 425	Val 410 Gly	395 Glu Glu	Trp Ser Lys	Glu Gly	Glu Glu 430	Ile 415 Glu	400 Lys Leu
385 Arg Arg	Met Val Cys	Arg Ile Asn 435	Ile Glu 420 Ala	Asn 405 Leu Lys	390 Glu Val Lys	Gln Asp Met	Gly Asp Lys 440	Val Gly 425 Glu	Val 410 Gly Leu	395 Glu Glu Ala	Trp Ser Lys Arg	Glu Gly Glu 445	Glu Glu 430 Ala	Ile 415 Glu Val	400 Lys Leu Lys
385 Arg Arg	Met Val Cys	Arg Ile Asn 435	Ile Glu 420 Ala	Asn 405 Leu Lys	390 Glu Val Lys	Gln Asp Met Trp	Gly Asp Lys 440	Val Gly 425 Glu	Val 410 Gly Leu	395 Glu Glu Ala	Trp Ser Lys Arg	Glu Gly Glu 445	Glu Glu 430 Ala	Ile 415 Glu Val	400 Lys Leu Lys
385 Arg Arg Arg	Met Val Cys Lys	Arg Ile Asn 435 Gly	Ile Glu 420 Ala Ser	Asn 405 Leu Lys	390 Glu Val Lys	Gln Asp Met Trp Lys	Gly Asp Lys 440	Val Gly 425 Glu	Val 410 Gly Leu	395 Glu Glu Ala	Trp Ser Lys Arg	Glu Gly Glu 445	Glu Glu 430 Ala	Ile 415 Glu Val	400 Lys Leu Lys

Sequence

Sequence ID No.:

Sequence length:

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1507

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Num	ber	of	str	and	s:	Dou	ble	-sti	cand							
Тор	olo	gy:	St	rai	ght	cha	in									
Sou	rce	:														
	В	iolo	ogic	al	name	e :	Per	illá	a (P	eri	lla	fru	tes	cens	5)	
	T .	issı	ıe t	ype	: I	Leaf										
Dir	ect	sou	ırce	::												
	L	ibra	ary	nam	e:	cDN	A 1	ibra	ary							
	C.	lone	e na	me:	p.	3R4										
_	uen															
GAAA	AATT	rcc A	ACAAA	AA A?	rg g:	rc co	GC CC	GC CC	GC G	rg Ci	rg Ci	ra Go	CA AC	CG T	ГT	49
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				AAC												337
Glu	Ala	Leu	Arg	Asn	Leu	Leu	Leu	Asn	Asn	His	Asp	Val	Thr	Phe	Val	
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Ile	Val	Ser	Trp	Cys	Ser	Gln	Leu	Glu	Va1	Leu	Ala	His	Pro	Ala	Leu	
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Val	G1u	Met	Val	Met	Asp	Gly	Gly	Glu	Lys	Ser	Lys	Leu	Val	Arg	Glu	
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Gly	Ser	Ser	Leu	Lys	Asn	Leu	Asn	Ala	Phe	Leu	His	Gln	Val	Ala	Arg	
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GCT	TAA	CACAC	CAA A	AATG	GCTT	rc ca	ACTT	CAAT	CTA	ACTCA	AAAC	ACC	GTT(CAA		1446
Ala																
460	,															1507
ATA	AATA!	rcc c	CCTT	CCAC	rr ci	TTCT	TATT	CAC	CTATO	CACA	TTTA	AATA	TTT	TAGTA	AACAAA	1506
Α																
500		aa 1	r n		2											

Sequence ID No.: 2

Sequence length: 1470

Double-strand

Nucleic acid

Sequence type:

Number of strands:

Topology: Straight chain

Source: Perilla (Perilla frutescens) Biological name: Tissue type: Leaf Direct source: cDNA library Library name: Clone name: p3R6 Sequence: ACCAAACCAA AACAAAATTT CCACAAAA ATG GTC CGC CGC CGC GTG CTG CTA 48 Met Val Arg Arg Arg Val Leu Leu 5 1 GCA ACG TTT CCG GCG CAA GGC CAC ATA AAT CCC GCC CTC CAA TTC GCC 96 Ala Thr Phe Pro Ala Gln Gly His Ile Asn Pro Ala Leu Gln Phe Ala 15 AAG AGA CTC CTA AAA GCC GGC ACT GAC GTC ACG TTT TTC ACG AGC GTT 144 Lys Arg Leu Leu Lys Ala Gly Thr Asp Val Thr Phe Phe Thr Ser Val 35 30 25 TAT GCA TGG CGC CGC ATG GCC AAC ACA GCC TCC GCC GCT GCC GGA AAC 192 Tyr Ala Trp Arg Arg Met Ala Asn Thr Ala Ser Ala Ala Gly Asn 55 45 CCA CCG GGC CTC GAC TTC GTG GCG TTC TCC GAC GGC TAC GAC GGG 240 Pro Pro Gly Leu Asp Phe Val Ala Phe Ser Asp Gly Tyr Asp Asp Gly 65 60 CTG AAG CCC GGC GGC GAC GGG AAG CGC TAC ATG TCC GAG ATG AAA GCC 288 Leu Lys Pro Gly Gly Asp Gly Lys Arg Tyr Met Ser Glu Met Lys Ala 85 75 80 336 CGC GGC TCC GAG GCC TTA AGA AAC CTC CTT CTC AAC AAC GAC GAC GTC Arg Gly Ser Glu Ala Leu Arg Asn Leu Leu Leu Asn Asn Asp Asp Val 95 ACT TTC GTC GTC TAC TCC CAC CTC TTT GCA TGG GCG GCG GAG GTG GCG 384 Thr Phe Val Val Tyr Ser His Leu Phe Ala Trp Ala Ala Glu Val Ala 120 105 110 115

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GTG	CTG	TGC	ATA	TAC	CAC	TTC	TAC	TTC	AAC	GGC	TAC	GCA	GAC	GAG	ATC	480
Va1	Leu	Cys	lle	Tyr	His	Phe	Tyr	Phe	Asn	G1y	Tyr	Ala	Asp	Glu	Ile	
			140					145					150			
GAC	GCC	GGT	TCC	AAT	GAA	ATT	CAG	CTC	CCT	CGG	CTT	CCA	TCC	CTG	GAG	528
Asp	Ala	Gly	Ser	Asn	G1u	Ile	Gln	Leu	Pro	Arg	Leu	Pro	Ser	Leu	Glu	
		155					160					165				
CAG	CGC	AGT	CTT	CCG	ACG	TTT	CTG	CTG	CCT	GCG	ACG	CCG	GAG	AGA	TTC	576
G1n	Arg	Ser	Leu	Pro	Thr	Phe	Leu	Leu	Pro	Ala	Thr	Pro	G1u	Arg	Phe	
	170					175					180					
CGG	TTG	ATG	ATG	AAG	GAG	AAG	CTG	GAA	ACT	TTA	GAC	GGT	GAA	GAG	AAG	624
Arg	Leu	Met	Met	Lys	Glu	Lys	Leu	Glu	Thr	Leu	Asp	Gly	Glu	Glu	Lys	
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GCG	AAA	GTA	TTG	GTG	AAC	ACG	TTT	GAT	GCG	TTG	GAG	CCC	GAT	GCA	CTC	672
Ala	Lys	Va1	Leu	Va1	Asn	Thr	Phe	Asp	Ala	Leu	Glu	Pro	Asp	Ala	Leu	
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ACG	GCT	ATT	GAT	AGG	TAT	GAG	TTG	ATC	GGG	ATC	GGG	CCG	TTG	ATT	CCC	720
Thr	A1a	Ile	Asp	Arg	Tyr	Glu	Leu	Ile	Gly	Ile	Gly	Pro	Leu	Ile	Pro	
			220					225					230			
TCC	GCC	TTC	TTG	GAC	GGC	GAA	GAT	CCC	TCC	GAA	ACG	TCT	TAC	GGC	GGC	768
Ser	Ala	Phe	Leu	Asp	Gly	Glu	Asp	Pro	Ser	Glu	Thr	Ser	Tyr	G1y	G1y	
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GAT	CTT	TTC	GAA	AAA	TCG	GAG	GAG	AAT	AAC	TGC	GTG	GAG	TGG	TTG	AAC	816
Asp	Leu	Phe	G1u	Lys	Ser	Glu	Glu	Asn	Asn	Cys	Val	Glu	Trp	Leu	Asn	
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Ser	Lys	Pro	Lys	Ser	Ser	Val	Va1	Tyr	Val	Ser	Phe	Gly	Ser	Val	Leu	
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Arg	Phe	Pro	Lys	Ala	Gln	Met	G1u	Glu	Ile	G1y	Lys	Gly	Leu	Leu	Ala	
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TGC	GGA	AGG	ccc	TTT	TTA	TGG	ATG	ATA	CGA	GAA	CAG	AAG	AAT	GAC	GAC	960
Cys	G1y	Arg	Pro	Phe	Leu	Trp	Met	Ile	Arg	Glu	G1n	Lys	Asn	Asp	Asp	
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315 320 325														
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Lys Lys Met Gly Lys Ile Val Ser Trp Cys Ser Gln Leu Glu Val Leu														
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Lys Leu Val Arg Glu Asn Ala Ile Lys Trp Lys Thr Leu Ala Arg Gln														
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GCC ATG GGA TAGGATGGAT CTTCACTCAA CAATCTCAAC GCCTTTCTTC 1393														
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Sequence length: 2062														
Sequence type: Nucleic acid														
Number of strands: Double-strand														

Number of strands: Double-strand

Topology: Straight chain

Source:

Biological name: Verbena (Verbena hybrida)

Tissue type: Petal

Direct source:

Library name: cDNA library

Clone name: pSHGT8

Cione name: pondi	o .	
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CGT CTC GCA AAT GCC GAC ATT	CAA GTC ACA TTC TT	TC ACC AGC GTC TAC 148
Arg Leu Ala Asn Ala Asp Ile	Gln Val Thr Phe Ph	e Thr Ser Val Tyr
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Ala Trp Arg Arg Met Ser Arg	Thr Ala Ala Gly Se	r Asn Gly Leu Ile
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GCC TTG AGC GAT ACT CTT GCA	GCC AAT AAT GTC GA	AT CAA AAA AGC AGC 340
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AAA ATC ACG TTC GTG GTG TAC	TCC CAC CTC TTT GC	CA TGG GCG GCC AAG 388
Lys Ile Thr Phe Val Val Tyr	Ser His Leu Phe Al	a Trp Ala Ala Lys
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GTG GCG CGT GAG TTC CAT CTC	CGG AGC GCG CTA CT	CC TGG ATT GAG CCA 436
Val Ala Arg Glu Phe His Leu	Arg Ser Ala Leu Le	u Trp Ile Glu Pro
125	130	135
GCT ACG GTG TTG GAT ATA TTT	TAC TTT TAT TTC AA	AC GGC TAT AGC GAC 484
Ala Thr Val Leu Asp Ile Phe	Tyr Phe Tyr Phe As	n Gly Tyr Ser Asp
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Secondary Seco	GAA	ATC	GAT	GCG	GGT	TCG	GAT	GCT	ATT	CAC	TTG	ccc	GGA	GGA	CTC	CCA	532
State Stat	Glu	Ile	Asp	Ala	Gly	Ser	Asp	Ala	Ile	His	Leu	Pro	G1y	Gly	Leu	Pro	
Val Leu Ala Gln Arg Asp Asp Leu Pro Ser Phe Leu Leu Pro Ser Thr His 175 185 185 GAG AGA TTC CGT TCA CTG ACG AGG AAG AGG AAA TTG GAA ACT TTA GAA GGT GER AGG AGA ARG TTG GAG AGG AAA TTG GAA ACT TTA GAA GGT GER AGG AGA AGA GAA AGA CT TA GAA GGT GER AGG AGA AAA CT AGG TTG GAG AGA GAA AAA CT AAG GTC TA GAG GTG AGG AGG TTG GAG CCT AGG GAG AGA AAA CCT AAG GTC TA GAG AGG AGG TTG GAG AGG TTG GAG AGG AG		155					160					165					
170	GTG	CTG	GCC	CAG	CGT	GAT	TTA	CCG	TCT	TTC	CTT	CTT	CCT	TCC	ACG	CAT	580
GAG AGA TTC CGT TCA CTG ATG AAG GAG AAA TTG GAA ACT TTA GAA GGT 628 Glu Arg Phe Arg Ser Leu Met Lys Glu Lys Leu Glu Thr Leu Glu Gly 190 195 200 GAA GAA AAA CCT AAG GTC TTG GTG AAC AGC TTT GAT GCT GAG CCT 676 Glu Glu Lys Pro Lys Val Leu Val Asn Ser Phe Asp Ala Leu Glu Pro 205 210 215 GAT GCG CTC AAG GCC ATT GAT AAG TAC GAG ATG GTG ATT GAT GCA ATC GGG CCG 724 Asp Ala Leu Lys Ala Ile Asp Lys Tyr Glu Met Ile Ala Ile Gly Pro 220 225 225 230 TTG ATT CCT TCC GCA TTC TTG GAC GGT AAA GAT CCT TCG GAC AGG TCT 772 Leu Ile Pro Ser Ala Phe Leu Asp Gly Lys Asp Pro Ser Asp Arg Ser 235 240 250 245 TTC GGC GGA GAT TTG TTC GAG AAA GGG TCG AAT GAC GAC GAT TGC CTC 820 Phe Gly Gly Asp Leu Phe Glu Lys Gly Ser Asn Asp Asp Asp Cys Leu 250 255 266 267 CGA AGG CCT CGA AGG TCT TCG GAC AGG TCT 772 GAA TGG TTG AGC AGC AAT CCT CGA TCC TGG GAC AGG TCT TGG GTG TTC ASP GAA TGG TTG AGC ACG AAT CCT CGA TCC TGG GTG TTC TGG GTG TTC TCG GAC AGG TCT 772 GAA TGG TTG AGC AGC AAT CCT CGA TCC TGG GTG TTC TGG GTG TTC TCG GAC AGG TCT 772 GAA TGG TTG AGC ACG AAT CCT CGA TCT TCG GTG GTT TAC GTT TCG TTC 868 Glu Trp Leu Ser Thr Asn Pro Arg Ser Ser Val Val Tyr Val Ser Phe 270 270 275 280 GGA AGC TTC GTT AAT ACG ACG AAG TCG CAA ATG GAC GAC GAT GCA AGA 916 Gly Ser Phe Val Asn Thr Thr Lys Ser Gln Met Glu Glu Ile Ala Arg 285 290 295 GGG CTG TTA GAT TGT GGG AGG CCG TTT TGT TGG GTG GTA AGA GAG GTA AAC GIY Leu Leu Asp Cys Gly Arg Pro Phe Leu Trp Val Val Arg Val Asn	Val	Leu	Ala	Gln	Arg	Asp	Leu	Pro	Ser	Phe	Leu	Leu	Pro	Ser	Thr	His	
Call	170					175					180					185	
195 200 676	GAG	AGA	TTC	CGT	TCA	CTG	ATG	AAG	GAG	AAA	TTG	GAA	ACT	TTA	GAA	GGT	628
GAA GAA AAA CCT AAG GTC TTG GTG AAC AGC TTT GAT GCG TTG GAG CCT GTG GAG GAC AGA AAA CCT AAG GTC TTG GTG AAC AGC TTT GAT GCG TTG GAG CCT GAG GCG GTG GAG GCG Ly Sproken and the second state of the second stat	G1u	Arg	Phe	Arg	Ser	Leu	Met	Lys	G1u	Lys	Leu	Glu	Thr	Leu	Glu	G1y	
C1u C1u Lys Pro Lys Val Leu Val Asn Ser Phe Asp Ala Leu C1u Pro 205 210 215 215 215 216 215 216 215 216 216 216 216 216 216 217 218					190					195					200		
GAT GCG CTC AAG GCC ATT GAT AAG TAC GAG ATT GCA ATG ATG GCA ATT GCG CCG 724 ASP A1a Leu Lys A1a Ile Asp Lys Tyr Glu Met Ile A1a Ile Gly Pro 230 772 772 TTG ATT CCT TCC GCA TTC TTG GAC GGT AAA GAT CCT TCG GAG ATT 772 Leu Ile Pro Ser Ala Phe Leu Asp GGT AAA GAT CCT TCG AGG AGG TCT 772 Leu Ile Pro Ser Ala Phe Leu Asp GGT AGG A	GAA	GAA	AAA	CCT	AAG	GTC	TTG	GTG	AAC	AGC	TTT	GAT	GCG	TTG	GAG	CCT	676
GAT GCG CTC AAG GCC ATT GAT AAG TAC GAG ATG ATT GCA ATC GGG CCG Asp Ala Leu Lys Ala Ile Asp Lys Tyr Glu Met Ile Ala Ile Gly Pro 220 225 230 TTG ATT CCT TCC GCA TTC TTG GAC GGT AAA GAT GAT GAT GAT AGA AGA GAT AGA GAT AGA AGA	G1u	Glu	Lys	Pro	Lys	Va1	Leu	Val	Asn	Ser	Phe	Asp	Ala	Leu	Glu	Pro	
Asp Ala Leu Lys Ala 11e Asp Lys Tyr Glu Met 11e Ala 11e Gly Pro 220 225 230 230 772 TTG ATT CCT TCC GCA TTC TTG GAC GCA TTC TTG GAC GCA ATT TTG GAC GCA ATT TTG GAC GAC AGG TCT TCG GAC AGG TCT AAA GAT GAC GAC GAC AGG TCT ASp Arg Ser 245 245 245 826 827 820 </td <td></td> <td></td> <td></td> <td>205</td> <td></td> <td></td> <td></td> <td></td> <td>210</td> <td></td> <td></td> <td></td> <td></td> <td>215</td> <td></td> <td></td> <td></td>				205					210					215			
TTG ATT CCT TCC GCA TTC TTG GAC GGT AAA GAT CCT TCG GAC AGG TCT TTG ATT CTG GGC GGA AAA GAT CCT TCG GAC AGG TCT TTG CTG GAC AAA GGT TTG CTG CTG CTG CTG CTG GAC AAA GGG TCG AAT GAC GAC GAT TGC CTC TTG CTG CTG CTG CTG AAA TGG CTG AAA TGG CTG AAA TGG CTG CTG AAA TGG CTG CTG AAA TGG CTG CTG CTG CTG CTG CTG CTG CTG CTG	GAT	GCG	CTC	AAG	GCC	ATT	GAT	AAG	TAC	GAG	ATG	ATT	GCA	ATC	GGG	CCG	724
TTG ATT CCT TCC GCA TTC TTG GAC GGT AAA GAT CCT TCG GAC AGG TCT 772 Leu 11e Pro Ser Ala Phe Leu Asp Gly Lys Asp Pro Ser Asp Arg Ser 235 TTC GGC GGA GAT TTG TTC GAG AAA GGG TCG AAT GAC GAC GAT TGC CTC 820 Phe Gly Gly Asp Leu Phe Glu Lys Gly Ser Asp Asp Asp Cys Leu 250 GAA TGG TTG AGC ACG AAT CCT CGA TCT TCG GTG GTT TAC GTT TCG TTC 265 GAA TGG TTG AGC ACG AAT CCT CGA TCT TCG GTG GTT TAC GTT TCG TTC 266 Glu Trp Leu Ser Thr Asn Pro Arg Ser Ser Val Val Tyr Val Ser Phe 270 GGA AGC TTC GTT AAT ACG ACG AAG TCG CAA ATG GAA GAG ATA GCA AGA 916 Gly Ser Phe Val Asn Thr Thr Lys Ser Gln Met Glu Glu Ile Ala Arg 285 GGG CTG TTA GAT TGT GGG AGG CCG TTT TTG TGG GTG GTA AGA GTA AAC 964 Gly Leu Leu Asp Cys Gly Arg Pro Phe Leu Trp Val Val Arg Val Asn	Asp	Ala	Leu	Lys	Ala	Ile	Asp	Lys	Tyr	Glu	Met	Ile	Ala	Ile	Gly	Pro	
Leu 11e Pro Ser Ala Ser Ala Sala Ser Ala Seg Ser Ala Sala Ser Ala Seg Ser Ala Seg Ser Ala Seg Ser Ser Ala Seg Ser			220					225					230				
TTC GGC GGA GAT TTC GAG AAA GGG TCG AAT GAC GAT TGC CTC 820 Phe G1y G1y Asp Leu Phe G1u Lys G1y Ser Asp Asp Asp Cys Leu 250 TTG AGC ACG AAT CCT CGA TCT TCG GTT TAC GTT TCG TTC 265 GAA TTG AGC ACG AAT CCT CGA TCT TCG GTT TAC GTT TCG TTC T	TTG	ATT	CCT	TCC	GCA	TTC	TTG	GAC	GGT	AAA	GAT	CCT	TCG	GAC	AGG	TCT	772
TTC GGC GGA GAT TTG TTC GAG AAA GGG TCG AAT GAC GAC GAT TGC CTC Phe Gly Gly Asp Leu Phe Glu Lys Gly Ser Asn Asp Asp Asp Cys Leu 250	Leu	Ile	Pro	Ser	Ala	Phe	Leu	Asp	Gly	Lys	Asp	Pro	Ser	Asp	Arg	Ser	
Phe Gly Gly Asp Leu Phe Glu Lys Gly Ser Asp Asp Asp Cys Leu 250 255 255 260 260 260 265 265 GAA TGG AGC AAC AAT CCT CGA TCT TCG GTT TAC GTT TCG TTC TTC TTC B68 Glu Trp Leu Ser Thr Asn Pro Arg Ser Ser Val Val Tyr Val Ser Phe GGA AGC TTC GTA AGA ATA GCA AGA PHe P		235					240					245					
250	TTC	GGC	GGA	GAT	TTG	TTC	GAG	AAA	GGG	TCG	AAT	GAC	GAC	GAT	TGC	CTC	820
GAA TGG TTG AGC ACG AAT CCT CGA TCT TCG GTG GTT TAC GTT TCG TTC Glu Trp Leu Ser Thr Asn Pro Arg Ser Ser Val Val Tyr Val Ser Phe 270 275 280 GGA AGC TTC GTT AAT ACG ACG AAG TCG CAA ATG GAA GAG ATA GCA AGA 916 Gly Ser Phe Val Asn Thr Thr Lys Ser Gln Met Glu Glu Ile Ala Arg 285 290 295 GGG CTG TTA GAT TGT GGG AGG CCG TTT TTG TGG GTG GTA AGA GTA AAC Gly Leu Leu Asp Cys Gly Arg Pro Phe Leu Trp Val Val Arg Val Asn	Phe	G1y	G1y	Asp	Leu	Phe	G1u	Lys	Gly	Ser	Asn	Asp	Asp	Asp	Cys	Leu	
Glu Trp Leu Ser Thr Asn Pro Arg Ser Ser Val Val Tyr Val Ser Phe 270	250					255					260					265	•
GGA AGC TTC GTT AAT ACG ACG AAG TCG CAA ATG GAA GAG ATA GCA AGA 916 G1y Ser Phe Val Asn Thr Thr Lys Ser Gln Met Glu Glu Ile Ala Arg 285 290 295 GGG CTG TTA GAT TGT GGG AGG CCG TTT TTG TGG GTG GTA AGA GTA AAC 964 G1y Leu Leu Asp Cys Gly Arg Pro Phe Leu Trp Val Val Arg Val Asn 964	GAA	TGG	TTG	AGC	ACG	AAT	CCT	CGA	TCT	TCG	GTG	GTT	TAC	GTT	TCG	TTC	868
GGA AGC TTC GTT AAT ACG ACG AAG TCG CAA ATG GAA GAG ATA GCA AGA 916 Gly Ser Phe Val Asn Thr Thr Lys Ser Gln Met Glu Glu Ile Ala Arg 285 290 295 GGG CTG TTA GAT TGT GGG AGG CCG TTT TTG TGG GTG GTA AGA GTA AAC 964 Gly Leu Leu Asp Cys Gly Arg Pro Phe Leu Trp Val Val Arg Val Asn	G1u	Trp	Leu	Ser	Thr	Asn	Pro	Arg	Ser	Ser	Va1	Va1	Tyr	Va1	Ser	Phe	
Gly Ser Phe Val Asn Thr Thr Lys Ser Gln Met Glu Glu Ile Ala Arg 285 290 295 GGG CTG TTA GAT TGT GGG AGG CCG TTT TTG TGG GTG GTA AGA GTA AAC Gly Leu Leu Asp Cys Gly Arg Pro Phe Leu Trp Val Val Arg Val Asn					270					275					280		•
285 290 295 GGG CTG TTA GAT TGT GGG AGG CCG TTT TTG TGG GTG GTA AGA GTA AAC 964 Gly Leu Leu Asp Cys Gly Arg Pro Phe Leu Trp Val Val Arg Val Asn	GGA	AGC	TTC	GTT	AAT	ACG	ACG	AAG	TCG	CAA	ATG	GAA	GAG	ATA	GCA	AGA	916
GGG CTG TTA GAT TGT GGG AGG CCG TTT TTG TGG GTG GTA AGA GTA AAC Gly Leu Leu Asp Cys Gly Arg Pro Phe Leu Trp Val Val Arg Val Asn	Gly	Ser	Phe	Va1	Asn	Thr	Thr	Lys	Ser	Gln	Met	Glu	G1u	Ile	Ala	Arg	
Gly Leu Leu Asp Cys Gly Arg Pro Phe Leu Trp Val Val Arg Val Asn				285					290					295			
	GGG	CTG	TTA	GAT	TGT	GGG	AGG	CCG	TTT	TTG	TGG	GTG	GTA	AGA	GTA	AAC	964
	Gly	Leu	Leu	Asp	Cys	G1y	Arg	Pro	Phe	Leu	Trp	Val	Va1	Arg	Val	Asn	
300 305 310			300					305					310				
GAA GGA GAA GAG GTA TTG ATA AGT TGC ATG GAG GAG TTG AAA CGA GTG 1012	GAA	GGA	GAA	GAG	GTA	TTG	ATA	AGT	TGC	ATG	GAG	GAG	TTG	AAA	CGA	GTG	1012
Glu Gly Glu Glu Val Leu Ile Ser Cys Met Glu Glu Leu Lys Arg Val	G1u	G1y	Glu	G1u	Val	Leu	Ile	Ser	Cys	Met	Glu	Glu	Leu	Lys	Arg	Val	
315 320 325		315					320					325					
GGG AAA ATT GTA TCT TGG TGT TCT CAA TTG GAA GTC CTG ACG CAT CCC 1060	GGG	AAA	ATT	GTA	TCT	TGG	TGT	TCT	CAA	TTG	GAA	GTC	CTG	ACG	CAT	CCC	1060
Gly Lys Ile Val Ser Trp Cys Ser Gln Leu Glu Val Leu Thr His Pro	G1y	Lys	Ile	Val	Ser	Trp	Cys	Ser	Gln	Leu	Glu	Val	Leu	Thr	His	Pro	
330 335 340 345	330					335					340					345	

1108 TCG TTG GGA TGT TTC GTG ACA CAC TGC GGG TGG AAT TCG ACT CTA GAG Ser Leu Gly Cys Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu Glu 355 350 AGT ATA TCT TTC GGG GTT CCG ATG GTG GCT TTT CCG CAG TGG TTC GAT 1156 Ser Ile Ser Phe Gly Val Pro Met Val Ala Phe Pro Gln Trp Phe Asp 365 CAA GGG ACG AAT GCG AAG CTG ATG GAG GAT GTG TGG AGG ACG GGT GTG 1204 Gln Gly Thr Asn Ala Lys Leu Met Glu Asp Val Trp Arg Thr Gly Val 390 385 380 AGA GTG AGA GCT AAT GAG GAG GGT AGC GTC GTT GAT GGT GAA ATT 1252 Arg Val Arg Ala Asn Glu Glu Gly Ser Val Val Asp Gly Asp Glu Ile 405 395 AGG AGA TGT ATT GAG GAG GTT ATG GAT GGG GGA GAA AAG AGT AGG AAA 1300 Arg Arg Cys Ile Glu Glu Val Met Asp Gly Glu Lys Ser Arg Lys 420 415 CTT AGA GAG AGT GCT GGC AAG TGG AAG GAT TTG GCA AGA AAA GCT ATG 1348 Leu Arg Glu Ser Ala Gly Lys Trp Lys Asp Leu Ala Arg Lys Ala Met 440 435 430 GAG GAA GAT GGA TCT TCA GTT AAC AAC CTC AAG GTC TTT CTT GAT GAG 1396 Glu Glu Asp Gly Ser Ser Val Asn Asn Leu Lys Val Phe Leu Asp Glu 455 GTT GTA GGT ATC TAAAGACGTA AATGAGGTCC CCATAGGCAA AATTGCAAAT 1448 Val Val Gly Ile 460 461 TTCATCTCGT AAGTTGAATA CTTTTTGGCT TTAATTTTGT TCGAGTTTGT TTTTCAAAAT 1508 TTATCTTGTA ATTTTACATT GAGTGTAAAT TTAGTCTGAT TTTAACTGGA AAAATATAAA 1568 ATTCATTGTT GAGACTCTTC ATCAAAATCA TCTGATTTCC TTTATTGTCT TGGTCAAAAT 1628 TCTCATATCA ATTGGAAAAA ATAAATTTCA AAATCGTCCA ATTTTGAACC AAGAAAGAAG 1688 TATAATTTGA CCAAAATAAT AAAAGGATTC AAGTGATCTT GATGAAGTGT CTGAGCGACG 1748 AGTTCTATAT TTTTCCACCG AATTTCTAAC GAGTTTTTGA ATTTTTTTTA GCCAAAATCG 1808 GACTAACTTT GTACAAAATG AAAAGTTATA TGATGAAATT TTAAAAAAACA AACTCAGACA 1868 ATAATAAAGC CCGAAAGTAG TAAAATTACC TGACGAAATT TGCAATTTCG CCTCCTATTT 1928 TAATTTTTTT GGTGTGTTTA ATAAATCGGT TATTTTACTT TTAATTAAAA TAAAAGTGAG 1988 ATGCATGATA GCTTGGTGAG TATATATGAG TTGATGGTAA TGTACGATAT TTTCTAAAAA 2048 2062 AAAA AAAAAAA

Sequence ID No.: 4

Sequence length: 1671

Nucleic acid

Double-strand

Sequence type:

Number of strands:

Topology: Straight chain Source: Biological name: Tissue type: Petal Direct source: Library name: cDNA library Clone name: pSTGT5 Sequence: AACACATAAA AAAAAATAA AAGAAGAAAT AATTAAAAAA AAAA ATG GTT AAC 53 Met Val Asn 1 AAA CGC CAT ATT CTA CTA GCA ACA TTC CCA GCA CAA GGC CAC ATA AAC 101 Lys Arg His Ile Leu Leu Ala Thr Phe Pro Ala Gln Gly His Ile Asn CCT TCT CTC GAG TTC GCC AAA AGG CTC CTC AAC ACC GGA TAC GTC GAC 149 Pro Ser Leu Glu Phe Ala Lys Arg Leu Leu Asn Thr Gly Tyr Val Asp 35 30 2.5 20 CAA GTC ACA TTC TTC ACG AGT GTA TAC GCA TTG AGA CGC ATG CGC TTC 197 Gln Val Thr Phe Phe Thr Ser Val Tyr Ala Leu Arg Arg Met Arg Phe 40 45 50 GAA ACC GAT CCG AGC AGC AGA ATC GAT TTC GTG GCA TKT YCA GAT TCT 245 Glu Thr Asp Pro Ser Ser Arg Ile Asp Phe Val Ala Xaa Xaa Asp Ser 60 55 TAC GAT GAT GGC TTA AAG AAA GGC GAC GAT GGC AAA AAC TAC ATG TCG 293 Tyr Asp Asp Gly Leu Lys Lys Gly Asp Asp Gly Lys Asn Tyr Met Ser 80 75 70 341 GAG ATG AGA AAG CGC GGA ACG AAG GCC TTA AAG GAC ACT CTT ATT AAG Glu Met Arg Lys Arg Gly Thr Lys Ala Leu Lys Asp Thr Leu Ile Lys CTC AAC GAT GCT GCG ATG GGA AGT GAA TGT TAC AAT CGC GTG AGC TTT 389 Leu Asn Asp Ala Ala Met Gly Ser Glu Cys Tyr Asn Arg Val Ser Phe 110 115 100 105

GTG	GTG	TAC	TCT	CAT	CTA	TTT	TCG	TGG	GCA	GCT	GAA	GTG	GCG	CGT	GAA	437
Val	Val	Tyr	Ser	His	Leu	Phe	Ser	Trp	Ala	Ala	G1u	Va1	Ala	Arg	Glu	
				120					125					130		
GTC	GAC	GTG	CCG	AGT	GCC	CTT	CTT	TGG	ATT	GAA	CCG	GCT	ACG	GTT	TTC	485
Val	Asp	Val	Pro	Ser	Ala	Leu	Leu	Trp	Ile	Glu	Pro	Ala	Thr	Val	Phe	
			135					140					145			
GAT	GTG	TAC	TAT	TTT	TAC	TTC	AAT	GGG	TAT	GCC	GAT	GAT	ATC	GAT	GCG	533
Asp	Val	Tyr	Tyr	Phe	Tyr	Phe	Asn	Gly	Tyr	Ala	Asp	Asp	I1e	Asp	Ala	
		150					155					160				
GGC	TCA	GAT	CAA	ATC	CAA	CTG	ccc	AAT	CTT	CCG	CAG	CTC	TCC	AAG	CAA	581
Gly	Ser	Asp	Gln	Ile	Gln	Leu	Pro	Asn	Leu	Pro	Gln	Leu	Ser	Lys	Gln	
	165					170					175					
GAT	CTC	ССС	TCT	TTC	CTA	CTC	CCT	TCG	AGC	CCC	GCG	AGA	TTC	CGA	ACC	629
Asp	Leu	Pro	Ser	Phe	Leu	Leu	Pro	Ser	Ser	Pro	Ala	Arg	Phe	Arg	Thr	
180					185					190					195	
CTA	ATG	AAA	GAA	AAG	TTC	GAC	ACG	CTC	GAC	AAA	GAA	CCG	AAA	GCG	AAG	677
Leu	Met	Lys	G1u	Lys	Phe	Asp	Thr	Leu	Asp	Lys	G1u	Pro	Lys	Ala	Lys	
				200					205					210		
GTC	TTG	ATA	AAC	ACG	TTC	GAC	GCA	TTA	GAA	ACC	GAA	CAA	CTC	AAA	GCC	725
Va1	Leu	Ile	Asn	Thr	Phe	Asp	Ala	Leu	Glu	Thr	G1u	Gln	Leu	Lys	Ala	
			215					220					225			
ATC	GAC	AGG	TAT	GAA	CTA	ATA	TCC	ATC	GGC	CCA	TTA	ATC	CCA	TCA	TCG	773
Ile	Asp	Arg	Tyr	G1u	Leu	Ile	Ser	Ile	Gly	Pro	Leu	Ile	Pro	Ser	Ser	
		230					235					240				
ATA	TTC	TCA	GAT	GGC	AAC	GAC	CCC	TCA	TCA	AGC	AAC	AAA	TCC	TAC	GGT	821
lle	Phe	Ser	Asp	G1y	Asn	Asp	Pro	Ser	Ser	Ser	Asn	Lys	Ser	Tyr	Gly	
	245					250					255					
GGA	GAC	CTC	TTC	AGA	AAA	GCC	GAT	GAA	ACT	TAC	ATG	GAC	TGG	CTA	AAC	869
G1y	Asp	Leu	Phe	Arg	Lys	Ala	Asp	Glu	Thr	Tyr	Met	Asp	Trp	Leu	Asn	
260				-	265					270					275	
TCA	AAA	ccc	GAA	TCA	TCG	GTC	GTT	TAC	GTT	TCG	TTC	GGG	AGC	CTC	CTG	917
Ser	Lys	Pro	Glu	Ser	Ser	Val	Va1	Tyr	Va1	Ser	Phe	Gly	Ser	Leu	Leu	
				280					285					290		
AGG	CTC	CCG	AAA	ccć	CAA	ATG	GAA	GAA	ATA	GCA	ATA	GGG	CTT	TCA	GAC	965
Arg	Leu	Pro	Lys	Pro	Gln	Met	Glu	Glu	Ile	Ala	Ile	Gly	Leu	Ser	Asp	
			295					300					305			

ACC	AAA	TCG	CCA	GTT	CTC	TGG	GTG	ATA	AGA	AGA	AAC	GAA	GAG	GGC	GAC	1013
Thr	Lys	Ser	Pro	Val	Leu	Trp	Va1	Ile	Arg	Arg	Asn	Glu	Glu	Gly	Asp	
		310					315					320				
GAA	CAA	GAG	CAA	GCA	GAA	GAA	GAA	GAG	AAG	CTG	CTG	AGC	TTC	TTT	GAT	1061
Glu	G1n	Glu	Gln	Ala	Glu	G1u	Glu	Glu	Lys	Leu	Leu	Ser	Phe	Phe	Asp	
	325					330					335					
CGT	CAC	GGA	ACT	GAA	CGA	CTC	GGG	AAA	ATC	GTG	ACA	TGG	TGC	TCA	CAA	1109
Arg	His	Gly	Thr	Glu	Arg	Leu	Gly	Lys	Ile	Val	Thr	Trp	Cys	Ser	Gln	
340					345					350					355	
TTG	GAT	GTT	CTG	ACG	CAT	AAG	TCG	GTG	GGA	TGC	TTC	GTG	ACG	CAT	TGC	1157
Leu	Asp	Va1	Leu	Thr	His	Lys	Ser	Val	G1y	Cys	Phe	Va1	Thr	His	Cys	
				360					365					370		
GGT	TGG	AAT	TCT	GCT	ATC	GAG	AGC	CTG	GCT	TGT	GGT	GTG	CCC	GTG	GTG	1205
Gly	Trp	Asn	Ser	Ala	Ile	G1u	Ser	Leu	Ala	Cys	Gly	Val	Pro	Va1	Va1	
			375					380					385			
TGC	TTT	CCT	CAA	TGG	TTC	GAT	CAA	GGG	ACT	AAT	GCG	AAG	ATG	ATC	GAA	1253
Cys	Phe	Pro	G1n	Trp	Phe	Asp	Gln	Gly	Thr	Asn	Ala	Lys	Met	Ile	Glu	
		390					395					400				
GAT	GTG	TGG	AGG	AGT	GGT	GTG	AGA	GTC	AGA	GTG	AAT	GAG	GAA	GGC	GGC	1301
Asp	Val	Trp	Arg	Ser	Gly	Va1	Arg	Val	Arg	Val	Asn	G1u	Glu	G1y	G1y	
	405					410					415					
GTT	GTT	GAT	AGG	CGT	GAG	ATT	AAG	AGG	TGC	GTC	TCG	GAG	GTT	ATA	AAG	1349
Val	Va1	Asp	Arg	Arg	Glu	Ile	Lys	Arg	Cys	Val	Ser	Glu	Val	Ile	Lys	
420					425					430					435	
AGT	CGA	GAG	TTG	AGA	GAA	AGC	GCA	ATG	ATG	TGG	AAG	GGT	TTG	GCT	AAA	1397
Ser	Arg	Glu	Leu	Arg	Glu	Ser	Ala	Met	Met	Trp	Lys	Gly	Leu	Ala	Lys	
				440					445					450		
GAA	GCT	ATG	GAT	GAA	GAA	CGT	GGA	TCA	TCA	ATG	AAC	AAT	CTG	AAG	AAT	1445
G1u	Ala	Met	Asp	Glu	G1u	Arg	Gly	Ser	Ser	Met	Asn	Asn	Leu	Lys	Asn	
			455					460					465			
TTT	ATT	ACT	AGG	ATT	ATT	AAT	GAA	AAT	GCC	TCA	TAAG	GTTG'	rac			1488
Phe	Ile	Thr	Arg	Ile	Ile	Asn	Glu	Asn	Ala	Ser						
		470					475			478						
															ATGTAT	1548
															GCCATG	1608
ATT	AAA1	ATA '	rata:	TTTT	AA AA	ATAA	ATAT'	r tte	CTAC'	TTAT	AAA	CTAA	AAA A	AAAA	AAAAA	1668
ATTTAAAATA TATATTTTAA AATAAATATT TTCTACTATT AAACTAAAAA AAAAAAAA											1671					

Sequence ID No.: Sequence length:

Sequence type: Nucleic acid Number of strands: Double-strand Straight chain Topology: Source: Perilla (Perilla frutescens) Biological name: Tissue type: Leaf Direct source: cDNA library Library name: Clone name: p8R6 Sequence: TTCAAAACTC ATAACGTGAT TGAGCTAATG TGCACATCTT CCTCTTCAAA GTCTACAGTG 60 TCATCCTACC AGCATCATCA TGATCAATCT CTTTATAATG AGGAGAATGG AGTAACAAGG 120 AGTGGGTTTT GTTACTCAGC TTCAACCTAC GTACGTACTA CTACTGACTC AACTCTCAAG 180 AGAATGAATA TAATATAAA TGGGCGATAG ATCTTTGTAG ATATGTAGGT GTAGCCTGCA 240 GGTGGTTAAT TAATTTCCGG TGTGGGAAAA TAAATAAATA AATAAATATA GCG ATG AGC 299 Met Ser 1 AGC AGC AGC AGA AGG TGG AGA GAG AAT GAG GGG ATG CGA AGG ACA 347 Ser Ser Ser Arg Arg Trp Arg Glu Asn Glu Gly Met Arg Arg Thr 5 10 15 TTG CTG GGG TTG GGT TTG GGG CAG TTG GTT TCT TTC GAT TTG GCT ATC 395 Leu Leu Gly Leu Gly Leu Gly Gln Leu Val Ser Phe Asp Leu Ala Ile 2.5 20 ATG ACC TIT TCT GCT TCT TTG GTT TCA ACC ACA GTG GAT GCA CCA CTT 443 Met Thr Phe Ser Ala Ser Leu Val Ser Thr Thr Val Asp Ala Pro Leu 50 45 40 3.5 ACT ATG TCG TTC ACT ACA TAC ACT GTT GTG GCC CTG CTC TAT GGA ACC 491 Thr Met Ser Phe Thr Thr Tyr Thr Val Val Ala Leu Leu Tyr Gly Thr 60 5.5 ATC TTG CTT TAC CGC CGC CAC AAA TTC TTG GTT CCA TGG TAC TGG TAT 539 Ile Leu Leu Tyr Arg Arg His Lys Phe Leu Val Pro Trp Tyr Trp Tyr 80 75 70

GCT CTC CTG GGG TTC GTG GAC GTC CAC GGC AAT TAT CTT GTT AAT AAA Ala Leu Leu Gly Phe Val Asp Val His Gly Asn Tyr Leu Val Asn Lys GCA TTC GAG TTG ACA TCG ATT ACG AGT GTG AGC ATA CTG GAT TGT TGG Ala Phe Glu Leu Thr Ser Ile Thr Ser Val Ser Ile Leu Asp Cys Trp ACA ATC GTG TGG TCC ATC ATC TTT ACA TGG ATG TTC CTA GGC ACA AAA Thr Ile Val Trp Ser Ile Ile Phe Thr Trp Met Phe Leu Gly Thr Lys TAC TCT GTA TAC CAG TTT GTC GGT GCT GCT ATT TGT GTA GGA GGC CTC Tyr Ser Val Tyr Gln Phe Val Gly Ala Ala Ile Cys Val Gly Gly Leu CTC CTC GTG CTT CTT TCC GAC TCA GGG GTC ACT GCT GCT GGT TCG AAT Leu Leu Val Leu Leu Ser Asp Ser Gly Val Thr Ala Ala Gly Ser Asn CCT CTT TTG GGT GAT TTT CTT GTC ATA ACA GGC TCT ATT TTG TTC ACA Pro Leu Leu Gly Asp Phe Leu Val Ile Thr Gly Ser Ile Leu Phe Thr CTC AGC ACT GTT GGT CAG GAA TAC TGC GTG AAG AGG AAA GAT CGT ATT Leu Ser Thr Val Gly Gln Glu Tyr Cys Val Lys Arg Lys Asp Arg Ile GAA GTA GTA GCA ATG ATC GGT GTA TTT GGT ATG CTC ATC AGT GCA ACC Glu Val Val Ala Met Ile Gly Val Phe Gly Met Leu Ile Ser Ala Thr GAG ATT ACT GTG CTG GAG AGG AAT GCC CTC TCA TCA ATG CAG TGG TCT Glu Ile Thr Val Leu Glu Arg Asn Ala Leu Ser Ser Met Gln Trp Ser ACT GGA CTT TTG GCA GCC TAT GTT GTT TAT GCA CTG TCC AGC TTC CTC Thr Gly Leu Leu Ala Ala Tyr Val Val Tyr Ala Leu Ser Ser Phe Leu TTC TGC ACA CTC ACC CCT TTT CTT CTC AAG ATG AGT GGC GCT GCA TTT Phe Cys Thr Leu Thr Pro Phe Leu Leu Lys Met Ser Gly Ala Ala Phe TTC AAT CTT TCC ATG CTT ACA TCT GAT ATG TGG GCT GTT GCA ATT AGG Phe Asn Leu Ser Met Leu Thr Ser Asp Met Trp Ala Val Ala Ile Arg

ACA	TTC	ATA	TAC	AAC	CAG	GAG	GTT	GAT	TGG	TTA	TAC	TAT	TTG	GCC	TTT	1163
Thr	Phe	Ile	Tyr	Asn	Gln	Glu	Val	Asp	Trp	Leu	Tyr	Tyr	Leu	Ala	Phe	
275					280					285					290	
TGT	CTC	GTT	GTT	GTT	GGA	ATA	TTC	ATA	TAT	ACA	AAA	ACA	GAG	AAG	GAT	1211
Cys	Leu	Va1	Val	Val	Gly	Ile	Phe	Ile	Tyr	Thr	Lys	Thr	Glu	Lys	Asp	
				295					300					305		
CCT	AAC	AAT	ACG	AGA	GCC	CTT	GAG	AAT	GGA	AAC	TTG	GAT	CAT	GAA	TAT	1259
Pro	Asn	Asn	Thr	Arg	Ala	Leu	Glu	Asn	Gly	Asn	Leu	Asp	His	G1u	Tyr	
			310					315					320			
AGT	CTC	CTT	GAG	GAT	CAA	GAT	GAC	ACA	CCA	AGA	AAA	CCA	TAG	CTAGO	CTT	1308
Ser	Leu	Leu	Glu	Asp	G1n	Asp	Asp	Thr	Pro	Arg	Lys	Pro				
		325					330					335				
TGC	CAC	AAT (CTTT	CATO	CA AC	CAGT	ATT7	ATA A	AATTO	CGTG	AGG	GGGA	GAG A	AGATO	CGAGAT	1368
ACTA	ATTA	AAT (GGAC	STCTA	AT TA	ATAT!	AGTTO	G GAG	GTT	TTG	TTTT	ratt1	TAT :	TAT	TGAGT	1428
AAA	AAAA	AΑ														1437

Sequence ID No.: 6

Sequence length: 2105

Sequence type: Nucleic acid

Number of strands: Double-strand

Topology: Straight chain

Source:

Biological name: Petunia

Tissue type: Leaf

Direct source:

Library name: cDNA library

Clone name: pSPGT1

Sequence:

AGTGAGCGCA	ACGCAATTAA	TGTGAGTTAG	CTCACTCATT	AGGCACCCCA	GGCTTTACAC	60
TTTATGCTTC	CGGCTCGTAT	GTTGTGTGGA	ATTGTGAGCG	GATAACAATT	TCACACAGGA	120
AACAGCTATG	ACCATGATTA	CGCCAAGCTC	GAAATTAACC	CTCACTAAAG	GGAACAAAAG	180
CTGGAGCTCC	ACGCGGTGGC	GGCCGCTCTA	GAACTAGTGG	ATCCCCCGGG	CTGCAGGAAT	240
TCCGTTGCTG	TCGCCACAAT	TTACAAACCA	AGAAATTAAG	CATCCCTTTC	CCCCCTTAA	300
AAAACATACA	AGTTTTTAAT	TTTTCACTAA	GCAAGAAAAT	ATG GTG CAG	G CCT CAT GTC	358
				Met Val Gl	n Pro His Val	

5

ATC TTA ACA ACA TTT CCA GCA CAA GGC CAT ATT AAT CCA GCA CTT CAA Ile Leu Thr Thr Phe Pro Ala Gln Gly His Ile Asn Pro Ala Leu Gln TTT GCC AAG AAT CTT GTC AAG ATG GGC ATA GAA GTG ACA TTT TCT ACA Phe Ala Lys Asn Leu Val Lys Met Gly Ile Glu Val Thr Phe Ser Thr AGC ATT TAT GCC CAA AGC CGT ATG GAT GAA AAA TCC ATT CTT AAT GCA Ser Ile Tyr Ala Gln Ser Arg Met Asp Glu Lys Ser Ile Leu Asn Ala CCA AAA GGA TTG AAT TTC ATT CCA TTT TCC GAT GGC TTT GAT GAA GGT Pro Lys Gly Leu Asn Phe Ile Pro Phe Ser Asp Gly Phe Asp Glu Gly TTT GAT CAT TCA AAA GAC CCT GTA TTT TAC ATG TCA CAA CTT CGT AAA Phe Asp His Ser Lys Asp Pro Val Phe Tyr Met Ser Gln Leu Arg Lys TGT GGA AGT GAA ACT GTC AAA AAA ATA ATT CTC ACT TGC TCT GAA AAT Cys Gly Ser Glu Thr Val Lys Lys Ile Ile Leu Thr Cys Ser Glu Asn GGA CAG CCT ATA ACT TGC CTA CTT TAC TCC ATT TTC CTT CCT TGG GCA Gly Gln Pro Ile Thr Cys Leu Leu Tyr Ser Ile Phe Leu Pro Trp Ala GCA GAG GTA GCA CGT GAA GTT CAC ATC CCT TCT GCT CTT TGG AGT Ala Glu Val Ala Arg Glu Val His Ile Pro Ser Ala Leu Leu Trp Ser CAA CCA GCA ACA ATA TTG GAC ATA TAT TAC TTC AAC TTT CAT GGA TAT Gln Pro Ala Thr Ile Leu Asp Ile Tyr Tyr Phe Asn Phe His Gly Tyr GAA AAA GCT ATG GCT AAT GAA TCC AAT GAT CCA AAT TGG TCC ATT CAA Glu Lys Ala Met Ala Asn Glu Ser Asn Asp Pro Asn Trp Ser Ile Gln CTT CCC GGG CTT CCA CTA CTG GAA ACT CGA GAT CTT CCT TCA TTT TTA Leu Pro Gly Leu Pro Leu Leu Glu Thr Arg Asp Leu Pro Ser Phe Leu CTT CCT TAT GGT GCA AAA GGG AGT CTT CGA GTT GCA CTT CCA CCA TTC Leu Pro Tyr Gly Ala Lys Gly Ser Leu Arg Val Ala Leu Pro Pro Phe

AAA	GAA	TTG	ATA	GAC	ACA	TTA	GAT	GCT	GAA	ACC	ACT	CCT	AAG	ATT	CTT	982
Lys	G1u	Leu	Ile	Asp	Thr	Leu	Asp	Ala	G1u	Thr	Thr	Pro	Lys	Ile	Leu	
	200					205					210					
GTG	AAT	ACA	TTT	GAT	GAA	TTA	GAG	CCT	GAG	GCA	CTC	AAT	GCA	ATT	GAA	1030
Val	Asn	Thr	Phe	Asp	G1u	Leu	G1u	Pro	G1u	Ala	Leu	Asn	Ala	Ile	Glu	
215					220					225					230	
GGT	TAT	AAG	TTT	TAT	GGA	ATT	GGA	CCG	TTG	ATT	CCT	TCT	GCT	TTC	TTG	1078
G1y	Tyr	Lys	Phe	Tyr	Gly	lle	G1y	Pro	Leu	Ile	Pro	Ser	Ala	Phe	Leu	
				235					240					245		
GGT	GGA	AAT	GAC	ССТ	TTA	GAT	GCT	TCA	ттт	GGT	GGT	GAT	CTT	TTT	CAA	1126
G1y	G1y	Asn	Asp	Pro	Leu	Asp	Ala	Ser	Phe	Gly	Gly	Asp	Leu	Phe	Gln	
			250					255					260			
AAT	TCA	AAT	GAC	TAT	ATG	GAA	TGG	TTA	AAC	TCA	AAG	CCA	AÁT	TCA	TCA	1174
Asn	Ser	Asn	Asp	Tyr	Met	G1u	Trp	Leu	Asn	Ser	Lys	Pro	Asn	Ser	Ser	
		265	-				270					275				
GTT	GTT	TAT	ATA	тст	TTT	GGG	AGT	CTA	ATG	AAT	CCA	TCT	ATT	AGC	CAA	1222
Val	Val	Tyr	Ile	Ser	Phe	G1y	Ser	Leu	Met	Asn	Pro	Ser	Ile	Ser	Gln	
	280					285					290					
ATG	GAG	GAG	ATA	TCA	AAA	GGG	TTG	ATA	GAC	АТА	GGA	AGG	CCG	TTT	TTA	1270
Met	G1u	Glu	Ile	Ser	Lys	G1y	Leu	Ile	Asp	Ile	G1y	Arg	Pro	Phe	Leu	
295					300					305					310	
TGG	GTG	ATA	AAA	GAA	AAT	GAA	AAA	GGC	AAA	GAA	GAA	GAG	AAT	AAA	AAG	1318
Trp	Val	I1e	Lys	Glu	Asn	G1u	Lys	G1y	Lys	Glu	Glu	G1u	Asn	Lys	Lys	
•			•	315					320					325		
CTT	GGT	TGT	ATT	GAA	GAA	TTG	GAA	AAA	ATA	GGA	AAA	ATA	GTT	CCA	TGG	1366
	G1y															
		•	330					335					340			
TGT	TCA	CAA	СТТ	GAA	GTT	СТА	AAA	CAT	CCA	TCT	TTA	GGA	TGT	ттт	GTT	1414
	Ser															
,		345					350					355				
тст	CAT		GGA	TGG	AAT	TCA	GCC	TTA	GAG	AGT	TTA	GCT	TGT	GGA	GTG	1462
	His															
	360	-	•	•		365					370					
CCA	GTT	GTG	GCA	TTT	CCT		TGG	ACA	GAT	CAA	ATG	ACA	AAT	GCC	AAA	1510
	Val															
375					380				•	385					390	
										-						

CAA	GTT	GAA	GAT	GTG	TGG	AAA	AGT	GGA	GTA	AGA	GTG	AGA	ATA	AAT	GAA	1558
Gln	Va1	Glu	Asp	Va1	Trp	Lys	Ser	G1y	Val	Arg	Va1	Arg	Ile	Asn	Glu	
				395					400					405		
GAT	GGT	GTT	GTT	GAA	AGT	GAG	GAA	ATC	AAA	AGG	TGT	ATT	GAA	TTG	GTA	1606
Asp	G1y	Val	Va1	G1u	Ser	G1u	Glu	Ile	Lys	Arg	Cys	Ile	Glu	Leu	Va1	
			410					415					420			
ATG	GAT	GGA	GGA	GAG	AAA	GGG	GAA	GAA	TTG	AGA	AAG	AAT	GCT	AAG	AAA	1654
Met	Asp	Gly	Gly	G1u	Lys	G1y	Glu	Glu	Leu	Arg	Lys	Asn	Ala	Lys	Lys	
		425					430					435				
TGG	AAA	GAA	TTG	GCT	AGA	GAA	GCT	GTG	AAG	GAA	GGT	GGA	TCT	TCA	CAC	1702
Trp	Lys	G1u	Leu	Ala	Arg	Glu	Ala	Val	Lys	G1u	G1y	Gly	Ser	Ser	His	
	440					445					450					
AAG	AAT	TTA	AAG	GCT	TTT	ATT	GAT	GAT	GTT	GCC	AAA	GGG	TTT	TAAT	TATTTAC	1754
Lys	Asn	Leu	Lys	Ala	Phe	Ile	Asp	Asp	Val	Ala	Lys	Gly	Phe			
455					460					465			468			
AGG	сттт	rgc (CGTGA	TAT	ra ci	TCCC	CTA	TTC	GCGA	ATTC	ACTO	CTTT	STG (GACT	TGCTTG	1814
ACAA	AAAA	ACT (GAGGO	SAAT	T GO	CTAAC	ACAC	GC1	TAAT	CTT	TAAC	GAAG1	CA	rttco	CAAGGC	1874
TTGA	AGCC	CTG (СТТТ	AAAa	AC TI	ATTA	AGCC#	A GTA	AATCI	ATA	GGG1	тсто	CTT (CTAT	гтттст	1934
CTGT	CTCI	CT :	TTTT#	AGCCI	rr TI	TCT	TCCA	A AGO	STTTA	AAGA	ATAC	CGT	GAA (CATAC	GCTTAG	1994
TACC	TAGT	CT 1	rggt <i>i</i>	ATCTO	T A	CTTA	CCA	A GTO	GCAA	ATT	ATG	CTTAT	rgc 1	rgtco	CTCCTA	2054
ΔΔΤΊ	יייכייי	ר א א י	ΓΔΑΑΑ	TGCA	A G	TGA	AAAG	TAC	CAAAA	AAA	AAAA	AAAA	AAA A	4		2105